

SEQUENCE LISTING

<110> JAWORSKI, DEBORAH DEE
PAYNE, DAVID J.
SLATER-RADOSTI, COURTNEY E.
YAN, KANG

<120> METHODS OF MODULATING ACTIVITY OF DXR

<130> GM50074

<140> TO BE ASSIGNED

<141> 2001-08-09

<150> 60/223,909

<151> 2000-08-09

<160> 6

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1191

<212> DNA

<213> Haemophilus influenzae

<400> 1

```
atgcaaaaac aaaacattgt cattcttgggt tcaacgggat caatcggtaa gagtaccctt 60
tctgttatcg aaaataaccc tcagaaatat catgcatttg cactcgtagg cggaaaaaat 120
gtagaagcaa tgtttgaaca atgtatcaaa ttccgaccgc actttgcggc tcttgatgat 180
gtaaattgcgg ctaaaatttt acgtgaaaaa ttaattgcgc atcatattcc aacggaagta 240
ttagcaggac gacgagctat ttgcgaactc gcagcacacc cagatgccga tcagataatg 300
gcgtcgattg ttggtgcagc aggattgtta ccgactcttt cagcgggttaa agcaggtaaa 360
cgggtattac tggcaaataa agaatacactg gtaacctgcg gacagctttt tattgatgcc 420
gtaaaaaact atggctcgaa gcttttacca gtagatagtg aacataatgc tatctttcaa 480
tcattaccgc cagaagcaca agaaaaaatc ggtttttgcc cactttctga attaggtgta 540
agtaaaatta tactcactgg ttctggcgga ccattccgtt acacgccact tgaacaattc 600
accaacataa caccagaaca agcggttgca caccctaatt ggtctatggg taaaaaaatt 660
```

0925778-080901

tctgtcgatt cagctacaat gatgaataag ggcttggaa acattgaggc tcgctggctt 720
 ttcaatgcaa gtgcggaaga aatggaagtt attattcatc cacaatcaat tattcattct 780
 atggtacggt atgttgacgg ctcaatcatt actcaaattg gaaatccaga tatgcgtaca 840
 ccaattgcag aaactatggc atatcctcac cgcacttttg ctggagtaga accactcgat 900
 ttctttaaaa tcaaagaact gacatttatt gaacctgatt ttaatcgcta tccaaattta 960
 aaactggcta ttgatgcctt tgctgcggt caatatgcga caacagcaat gaatgcagct 1020
 aatgaaattg ccgtacaagc attttttagat cgtcaaattg gctttatgga tattgcaaaa 1080
 attaattcga aaacaattga gagaatttcg ccttatacca ttcaaatat tgatgatgta 1140
 ctcgaaattg atgcacaagc aagagagatt gcgaaaacac tacttagaga a 1191

<210> 2

<211> 1588

<212> PRT

<213> Haemophilus influenzae

<400> 2

Met Gln Lys Gln Asn Ile Val Ile Leu Gly Ser Thr Gly Ser Ile Gly
 1 5 10 15
 Lys Ser Thr Leu Ser Val Ile Glu Asn Asn Pro Gln Lys Tyr His Ala
 20 25 30
 Phe Ala Leu Val Gly Gly Lys Asn Val Glu Ala Met Phe Glu Gln Cys
 35 40 45
 Ile Lys Phe Arg Pro His Phe Ala Ala Leu Asp Asp Val Asn Ala Ala
 50 55 60
 Lys Ile Leu Arg Glu Lys Leu Ile Ala His His Ile Pro Thr Glu Val
 65 70 75 80
 Leu Ala Gly Arg Arg Ala Ile Cys Glu Leu Ala Ala His Pro Asp Ala
 85 90 95
 Asp Gln Ile Met Ala Ser Ile Val Gly Ala Ala Gly Leu Leu Pro Thr
 100 105 110
 Leu Ser Ala Val Lys Ala Gly Lys Arg Val Leu Leu Ala Asn Lys Glu
 115 120 125
 Ser Leu Val Thr Cys Gly Gln Leu Phe Ile Asp Ala Val Lys Asn Tyr
 130 135 140
 Gly Ser Lys Leu Leu Pro Val Asp Ser Glu His Asn Ala Ile Phe Gln
 145 150 155 160
 Ser Leu Pro Pro Glu Ala Gln Glu Lys Ile Gly Phe Cys Pro Leu Ser
 165 170 175
 Glu Leu Gly Val Ser Lys Ile Ile Leu Thr Gly Ser Gly Gly Pro Phe
 180 185 190

09925778-080901

0992578.080901

Arg	Tyr	Thr	Pro	Leu	Glu	Gln	Phe	Thr	Asn	Ile	Thr	Pro	Glu	Gln	Ala	195	200	205
Val	Ala	His	Pro	Asn	Trp	Ser	Met	Gly	Lys	Lys	Ile	Ser	Val	Asp	Ser	210	215	220
Ala	Thr	Met	Met	Asn	Lys	Gly	Leu	Glu	Tyr	Ile	Glu	Ala	Arg	Trp	Leu	225	230	235
Ala	Thr	Gly	Cys	Ala	Ala	Ala	Ala	Ala	Cys	Ala	Ala	Ala	Ala	Cys	Ala	245	250	255
Thr	Thr	Gly	Thr	Cys	Ala	Thr	Thr	Cys	Thr	Thr	Gly	Gly	Thr	Thr	Cys	260	265	270
Ala	Ala	Cys	Gly	Gly	Gly	Ala	Thr	Cys	Ala	Ala	Thr	Cys	Gly	Gly	Thr	275	280	285
Ala	Ala	Gly	Ala	Gly	Thr	Ala	Cys	Cys	Cys	Thr	Thr	Thr	Cys	Thr	Gly	290	295	300
Thr	Thr	Ala	Thr	Cys	Gly	Ala	Ala	Ala	Ala	Thr	Ala	Ala	Cys	Cys	Cys	305	310	315
Thr	Cys	Ala	Gly	Ala	Ala	Ala	Thr	Ala	Thr	Cys	Ala	Thr	Gly	Cys	Ala	325	330	335
Thr	Thr	Thr	Gly	Cys	Ala	Cys	Thr	Cys	Gly	Thr	Ala	Gly	Gly	Cys	Gly	340	345	350
Gly	Ala	Ala	Ala	Ala	Ala	Ala	Thr	Gly	Thr	Ala	Gly	Ala	Ala	Gly	Cys	355	360	365
Ala	Ala	Thr	Gly	Thr	Thr	Thr	Gly	Ala	Ala	Cys	Ala	Ala	Thr	Gly	Thr	370	375	380
Ala	Thr	Cys	Ala	Ala	Ala	Thr	Thr	Cys	Cys	Gly	Ala	Cys	Cys	Gly	Cys	385	390	395
Ala	Cys	Thr	Thr	Thr	Gly	Cys	Gly	Gly	Cys	Thr	Cys	Thr	Thr	Gly	Ala	405	410	415
Thr	Gly	Ala	Thr	Gly	Thr	Ala	Ala	Ala	Thr	Gly	Cys	Gly	Gly	Cys	Thr	420	425	430
Ala	Ala	Ala	Ala	Thr	Thr	Thr	Thr	Ala	Cys	Gly	Thr	Gly	Ala	Ala	Ala	435	440	445
Ala	Ala	Thr	Thr	Ala	Ala	Thr	Thr	Gly	Cys	Gly	Cys	Ala	Thr	Cys	Ala	450	455	460
Thr	Ala	Thr	Thr	Cys	Cys	Ala	Ala	Cys	Gly	Gly	Ala	Ala	Gly	Thr	Ala	465	470	475
Thr	Thr	Ala	Gly	Cys	Ala	Gly	Gly	Ala	Cys	Gly	Ala	Cys	Gly	Ala	Gly	485	490	495
Cys	Thr	Ala	Thr	Thr	Thr	Gly	Cys	Gly	Ala	Ala	Cys	Thr	Cys	Gly	Cys	500	505	510

Ala Gly Cys Ala Cys Ala Cys Cys Cys Ala Gly Ala Thr Gly Cys Cys
 515 520 525
 Gly Ala Thr Cys Ala Gly Ala Thr Ala Ala Thr Gly Gly Cys Gly Thr
 530 535 540
 Cys Gly Ala Thr Thr Gly Thr Thr Gly Gly Thr Gly Cys Ala Gly Cys
 545 550 555 560
 Ala Gly Gly Ala Thr Thr Gly Thr Thr Ala Cys Cys Gly Ala Cys Thr
 565 570 575
 Cys Thr Thr Thr Cys Ala Gly Cys Gly Gly Thr Thr Ala Ala Ala Gly
 580 585 590
 Cys Ala Gly Gly Thr Ala Ala Ala Cys Gly Gly Gly Thr Ala Thr Thr
 595 600 605
 Ala Cys Thr Gly Gly Cys Ala Ala Ala Thr Ala Ala Ala Gly Ala Ala
 610 615 620
 Thr Cys Ala Cys Thr Gly Gly Thr Ala Ala Cys Cys Thr Gly Cys Gly
 625 630 635 640
 Gly Ala Cys Ala Gly Cys Thr Thr Thr Thr Thr Ala Thr Thr Gly Ala
 645 650 655
 Thr Gly Cys Cys Gly Thr Ala Ala Ala Ala Ala Ala Cys Thr Ala Thr
 660 665 670
 Gly Gly Cys Thr Cys Gly Ala Ala Gly Cys Thr Thr Thr Thr Ala Cys
 675 680 685
 Cys Ala Gly Thr Ala Gly Ala Thr Ala Gly Thr Gly Ala Ala Cys Ala
 690 695 700
 Thr Ala Ala Thr Gly Cys Thr Ala Thr Cys Thr Thr Thr Cys Ala Ala
 705 710 715 720
 Thr Cys Ala Thr Thr Ala Cys Cys Gly Cys Cys Ala Gly Ala Ala Gly
 725 730 735
 Cys Ala Cys Ala Ala Gly Ala Ala Ala Ala Ala Ala Thr Cys Gly Gly
 740 745 750
 Thr Thr Thr Thr Thr Gly Cys Cys Cys Ala Cys Thr Thr Thr Cys Thr
 755 760 765
 Gly Ala Ala Thr Thr Ala Gly Gly Thr Gly Thr Ala Ala Gly Thr Ala
 770 775 780
 Ala Ala Ala Thr Thr Ala Thr Ala Cys Thr Cys Ala Cys Thr Gly Gly
 785 790 795 800
 Thr Thr Cys Thr Gly Gly Cys Gly Gly Ala Cys Cys Ala Thr Thr Cys
 805 810 815
 Cys Gly Thr Thr Ala Cys Ala Cys Gly Cys Cys Ala Cys Thr Thr Gly
 820 825 830

09925778.080901

Ala	Ala	Cys	Ala	Ala	Thr	Thr	Cys	Ala	Cys	Cys	Ala	Ala	Cys	Ala	Thr
835						840						845			
Ala	Ala	Cys	Ala	Cys	Cys	Ala	Gly	Ala	Ala	Cys	Ala	Ala	Gly	Cys	Gly
850						855						860			
Gly	Thr	Thr	Gly	Cys	Ala	Cys	Ala	Cys	Cys	Cys	Thr	Ala	Ala	Thr	Thr
865						870						875			
Gly	Gly	Thr	Cys	Thr	Ala	Thr	Gly	Gly	Gly	Thr	Ala	Ala	Ala	Ala	Ala
			885						890			895			
Ala	Ala	Thr	Thr	Thr	Cys	Thr	Gly	Thr	Cys	Gly	Ala	Thr	Thr	Cys	Ala
			900						905			910			
Gly	Cys	Thr	Ala	Cys	Ala	Ala	Thr	Gly	Ala	Thr	Gly	Ala	Ala	Thr	Ala
915						920						925			
Ala	Gly	Gly	Gly	Cys	Thr	Thr	Gly	Gly	Ala	Ala	Thr	Ala	Cys	Ala	Thr
930						935						940			
Thr	Gly	Ala	Gly	Gly	Cys	Thr	Cys	Gly	Cys	Thr	Gly	Gly	Cys	Thr	Thr
945						950						955			
Thr	Thr	Cys	Ala	Ala	Thr	Gly	Cys	Ala	Ala	Gly	Thr	Gly	Cys	Gly	Gly
			965						970			975			
Ala	Ala	Gly	Ala	Ala	Ala	Thr	Gly	Gly	Ala	Ala	Gly	Thr	Thr	Ala	Thr
			980						985			990			
Thr	Ala	Thr	Thr	Cys	Ala	Thr	Cys	Cys	Ala	Cys	Ala	Ala	Thr	Cys	Ala
995						1000						1005			
Ala	Thr	Thr	Ala	Thr	Thr	Cys	Ala	Thr	Thr	Cys	Thr	Ala	Thr	Gly	Gly
1010						1015						1020			
Thr	Ala	Cys	Gly	Gly	Thr	Ala	Thr	Gly	Thr	Thr	Gly	Ala	Cys	Gly	Gly
1025						1030						1035			
Cys	Thr	Cys	Ala	Gly	Thr	Cys	Ala	Thr	Thr	Ala	Cys	Thr	Cys	Ala	Ala
			1045						1050			1055			
Ala	Thr	Gly	Gly	Gly	Ala	Ala	Ala	Thr	Cys	Cys	Ala	Gly	Ala	Thr	Ala
			1060						1065			1070			
Thr	Gly	Cys	Gly	Thr	Ala	Cys	Ala	Cys	Cys	Ala	Ala	Thr	Thr	Gly	Cys
1075						1080						1085			
Ala	Gly	Ala	Ala	Ala	Cys	Thr	Ala	Thr	Gly	Gly	Cys	Ala	Thr	Ala	Thr
1090						1095						1100			
Cys	Cys	Thr	Cys	Ala	Cys	Cys	Gly	Cys	Ala	Cys	Thr	Thr	Thr	Thr	Gly
1105						1110						1115			
Cys	Thr	Gly	Gly	Ala	Gly	Thr	Ala	Gly	Ala	Ala	Cys	Cys	Ala	Cys	Thr
			1125						1130			1135			
Cys	Gly	Ala	Thr	Thr	Thr	Cys	Thr	Thr	Thr	Ala	Ala	Ala	Ala	Thr	Cys
			1140						1145			1150			

Ala	Ala	Ala	Gly	Ala	Ala	Cys	Thr	Gly	Ala	Cys	Ala	Thr	Thr	Thr	Ala
1155						1160						1165			
Thr	Thr	Gly	Ala	Ala	Cys	Cys	Thr	Gly	Ala	Thr	Thr	Thr	Thr	Ala	Ala
1170						1175						1180			
Thr	Cys	Gly	Cys	Thr	Ala	Thr	Cys	Cys	Ala	Ala	Ala	Thr	Thr	Thr	Ala
1185						1190						1195			
Ala	Ala	Ala	Cys	Thr	Gly	Gly	Cys	Thr	Ala	Thr	Thr	Gly	Ala	Thr	Gly
1205						1210						1215			
Cys	Cys	Thr	Thr	Thr	Gly	Cys	Thr	Gly	Cys	Gly	Gly	Gly	Thr	Cys	Ala
1220						1225						1230			
Ala	Thr	Ala	Thr	Gly	Cys	Gly	Ala	Cys	Ala	Ala	Cys	Ala	Gly	Cys	Ala
1235						1240						1245			
Ala	Thr	Gly	Ala	Ala	Thr	Gly	Cys	Ala	Gly	Cys	Thr	Ala	Ala	Thr	Gly
1250						1255						1260			
Ala	Ala	Ala	Thr	Thr	Gly	Cys	Cys	Gly	Thr	Ala	Cys	Ala	Ala	Gly	Cys
1265						1270						1275			
Ala	Thr	Thr	Thr	Thr	Thr	Ala	Gly	Ala	Thr	Cys	Gly	Thr	Cys	Ala	Ala
1285						1290						1295			
Ala	Thr	Thr	Gly	Gly	Cys	Thr	Thr	Thr	Ala	Thr	Gly	Gly	Ala	Thr	Ala
1300						1305						1310			
Thr	Thr	Gly	Cys	Ala	Ala	Ala	Ala	Ala	Thr	Thr	Ala	Ala	Thr	Thr	Cys
1315						1320						1325			
Gly	Ala	Ala	Ala	Ala	Cys	Ala	Ala	Thr	Thr	Gly	Ala	Gly	Ala	Gly	Ala
1330						1335						1340			
Ala	Thr	Thr	Thr	Cys	Gly	Cys	Cys	Thr	Thr	Ala	Thr	Ala	Cys	Cys	Ala
1345						1350						1355			
Thr	Thr	Cys	Ala	Ala	Ala	Ala	Thr	Ala	Thr	Thr	Gly	Ala	Thr	Gly	Ala
1365						1370						1375			
Thr	Gly	Thr	Ala	Cys	Thr	Cys	Gly	Ala	Ala	Ala	Thr	Thr	Gly	Ala	Thr
1380						1385						1390			
Gly	Cys	Ala	Cys	Ala	Ala	Gly	Cys	Ala	Ala	Gly	Ala	Gly	Ala	Gly	Ala
1395						1400						1405			
Thr	Thr	Gly	Cys	Gly	Ala	Ala	Ala	Ala	Cys	Ala	Cys	Thr	Ala	Cys	Thr
1410						1415						1420			
Thr	Ala	Gly	Ala	Gly	Ala	Ala	Phe	Asn	Ala	Ser	Ala	Glu	Glu	Met	Glu
1425						1430						1435			
Val	Ile	Ile	His	Pro	Gln	Ser	Ile	Ile	His	Ser	Met	Val	Arg	Tyr	Val
1445						1450						1455			
Asp	Gly	Ser	Val	Ile	Thr	Gln	Met	Gly	Asn	Pro	Asp	Met	Arg	Thr	Pro
1460						1465						1470			

Ile Ala Glu Thr Met Ala Tyr Pro His Arg Thr Phe Ala Gly Val Glu
 1475 1480 1485
 Pro Leu Asp Phe Phe Lys Ile Lys Glu Leu Thr Phe Ile Glu Pro Asp
 1490 1495 1500
 Phe Asn Arg Tyr Pro Asn Leu Lys Leu Ala Ile Asp Ala Phe Ala Ala
 1505 1510 1515 1520
 Gly Gln Tyr Ala Thr Thr Ala Met Asn Ala Ala Asn Glu Ile Ala Val
 1525 1530 1535
 Gln Ala Phe Leu Asp Arg Gln Ile Gly Phe Met Asp Ile Ala Lys Ile
 1540 1545 1550
 Asn Ser Lys Thr Ile Glu Arg Ile Ser Pro Tyr Thr Ile Gln Asn Ile
 1555 1560 1565
 Asp Asp Val Leu Glu Ile Asp Ala Gln Ala Arg Glu Ile Ala Lys Thr
 1570 1575 1580
 Leu Leu Arg Glu
 1585

<210> 3
 <211> 32
 <212> DNA
 <213> Escherichia coli

<400> 3
 ttatacatat gaagcaactc accattctgg gc

32

<210> 4
 <211> 35
 <212> DNA
 <213> Escherichia coli

<400> 4
 ttataggatc ctcagcttgc gagacgcac acctc

35

<210> 5
 <211> 34
 <212> DNA
 <213> Haemophilus influenzae

<400> 5

tatatacata tgcaaaaaca aaacattgtc attc

34

<210> 6

<211> 40

<212> DNA

<213> Haemophilus influenzae

<400> 6

tatataggat cctcattctc taagtagtgt ttctgcaatc

40

09925778.080901